(1) GENERAL INFORMATION:

- (i) APPLICANT: Hewick, Rodney M. Wang, Jack H. Wozney, John M. Celeste, Anthony J.
- (ii) TITLE OF INVENTION: Bone and Cartilage Inductive Proteins
- (iii) NUMBER OF SEQUENCES: 14
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02140
 - (V) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible

 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - (vi) CURRENT APPLICATION DATA;
 - (A) APPLICATION NUMBER; US 07/800,364
 - (B) FILING DATE: 26-NOV-1991
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kapinos / Ellen J.

 - (B) REGISTRATION NUMBER: 32,245
 (C) REFERENCE/DOCKET NUMBER: GI 5182A
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE 617-876-1170
 - (B) TELEFAX: /617-876-5851
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) /ORIGINAL SOURCE:
 - (F) TISSUE TYPE: Bone

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp 1 5 10 25

Val Ile Ala Pro Gln Gly Tyr

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Bos taurus
 - (F) TISSUE TYPE: Bone
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Ser Ala Thr Ser Val Zeu Tyr Tyr Asp Ser Ser Asn Asn Val Ile
1 5 10 15

Leu Arg

(2) INFORMATION FOR SEQ/ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI/SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Bos taurus
 - (F) TISSUE TYPE: Bone
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Cys Cys Ala Pro Thr Lys

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Bos taurus
 - (F) TISSUE TYPE: Bone
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:

Thr Asn Glu Leu Pro Pro Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp 10

Val His Gly Ser His Gly Arg 20

- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS; double
 - (D) TOPOLOGY: limear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL, NO
 - (iv) ANTI-SENSE; NO
 - (vi) ORIGINAL/SOURCE:
 - (A) ORGANISM: Bos taurus
 - (vii) IMMEDIATE SOURCE: (B) /CLONE: acc30
 - (viii) POSITION IN GENOME:
 - (C) UNITS: bp
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 25..57
 - (ki) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCGCGT GCTGTGCTCC GACC AAG CTG AGC GCC ACC TCC GTG CTC TAC Lys Leu Ser Ala Thr Ser Val Leu Tyr 1

51

TAC GAC AGCAGCAACA ATGTAATTCT AGA Tyr Asp 10

- (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 199 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Bos Taurus
 - (vii) IMMEDIATE SOURCE;
 - (A) LIBRARY: Bovine genomic
 - (B) CLONE: Lambda 9800-10
 - (viii) POSITION IN GENOME:
 - (C) UNITS: /bp
 - (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 30..199
 - (ix) FEATURÉ:
 - (A) NAME/KEY: intron
 - (B)/LOCATION: 1..29
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 30..179
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGCCCGCTGC CCCCTCCCGC CCCCGCCAG GTG CAC CTG CTG AAG CCG CAC GCG Val His Leu Lys Pro His Ala

53

GTC CCC AAG GCG TGC TGC GCG CCC ACC AAG CTG AGC GCC ACT TCC GTG 101 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val 10 CTC TAC TAC GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC CGC AAC 149 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn 25 30 ATG GTG GTC CGC GCC TGC GGC TGC CAC TGAGGCCCCA ACTCCACCGG 196 Met Val Val Arg Ala Cys Gly Cys His CAG 199 (2) INFORMATION FOR SEQ ID NO:8: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 49 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8: Val His Leu Leu Lys Pro His Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asm/ Met Val Val Arg Ala Cys Gly Cys His (2) INFORMATION FOR SEQ /ID NO:9: (i) SEQUENCE CHARÁCTERISTICS: (A) LENGTH:/172 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHÉTICAL: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Bos taurus

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME: (C) UNITS: bp

(A) LIBRARY: Bovine genomic
(B) CLONE: Lambda 9800-10

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	(A) LENGTH: 119 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)) MOLECULE TYPE: DNA (genomic)	
(iii)) HYPOTHETICAL: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Bos taurus	
(vii)) IMMEDIATE SOURCE: (A) LIBRARY: Bovine genous (B) CLONE: Lambda 9800-10	
(viii)) POSITION IN GENOME: (C) UNITS: bp	
(ix)) FEATURE: (A) NAME/KEY: exon (B) LOCATION: 2099	
(ix)) FEATURE: (A) NAME/KEY: intron (B) LOCATION: 119	
(ix)) FEATURE: (A) NAME/KEY: intron (B) LOCATION: 100.119	
(ix)) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 2299	
(xi)) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
CCCTTGCG	GTG TCCCCGCAGA C GAC GTC CAC GGC TCC CAC GGC CGG CAG GTG Asp Val His Gly Ser His Gly Arg Gln Val 1 5 10	51
TGC CGT Cys Arg	CGG CAC GAG CTG TAC GTG AGC TTC CAG GAC CTG GGC TGG CTG Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu 15 20 25	99
GTGAGTTC	CCG ACTCTCCTTT	119
(2) INF9	RMATION FOR SEQ ID NO:12:	
/((i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
/ (i	ii) MOLECULE TYPE: protein	-
/ (x	xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	

Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu (2) INFORMATION FOR SEQ ID NO:13: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1003 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (F) TISSUE TYPE: Human Heart (vii) IMMEDIATE SOURCE: (A) LIBRARY: Human heart ODNA library stratagene catalog #936208 (B) CLONE: hH38 (viii) POSITION IN GENOME: (C) UNITS: bp (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 8./850 (ix) FEATURE: (A) NAME/KEY: /mat_peptide (B) LOCATION; 427..843 (ix) FEATURE: (A) NAME/KEY: mRNA (B) LOCATION: 1..997 (xi) SEQUENÇÉ DESCRIPTION: SEQ ID NO:13: GAATTCC GAG CC/C CAT TGG AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC 49 Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile -135 -139/-130 CCG GCT GGG GAG GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG 97 Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val -125 -120 CCC AGC/ATC CAC CTG CTC AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG 145 Pro Ser Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln -105 GTG FTC CAG GAG CAG TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT 193 Val /Val Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp -90

CTT CAG ACG Leu Gln Thr -75	Leu Arg	GCT GGA Ala Gly	GAC GAG Asp Glu -70	GGC TGG Gly Trp	CTG GTG C Leu Val L -65	TG GAT eu Asp	GTC Val	241
ACA GCA GCC Thr Ala Ala -60	AGT GAC Ser Asp	TGC TGG Cys Trp -55	TTG CTG Leu Leu	AAG CGT Lys Arg	CAC AAG G His Lys A -50	AC CTG sp Leu	GGA Gly	289
CTC CGC CTC Leu Arg Leu -45	TAT GTG Tyr Val	GAG ACT Glu Thr -40	GAG GAT Glu Asp	GGG CAC Gly His -35	AGC GTG &	AT CCT sp Pro	GGC Gly -30	337
CTG GCC GGC Leu Ala Gly	CTG CTG Leu Leu -25	GGT CAA Gly Gln	CGG GCC Arg Ala	CCA CGC Pro Arg -20	TCC CAA C. Ser Gln-G	AG CCT ln Pro -15	TTC Phe	385
GTG GTC ACT Val Val Thr	TTC TTC Phe Phe -10	AGG GCC Arg Ala	AGT CCG Ser Pro -5	AGT CCC Ser Pro	ATC CGC A Ile Arg T	CC CCT hr Pro 1	CGG Arg	433
GCA GTG AGG Ala Val Arg 5								481
CCG CAG GCC Pro Gln Ala 20								529
CAC GGC CGG His Gly Arg	CAG GTC Gln Val 40	Cys Arg	CCG CAC Arg His	GAG CTC Glu Leu 45	TAC GTC A Tyr Val S	GC TTC er Phe 50	CAG Gln	577
GAC CTT GGC Asp Leu Gly								625
TAT TAC TGT Tyr Tyr Cys 70	Glu Gly	GAG TGC Elu Cys	TCC TTC Ser Phe 75	CCG CTG Pro Leu	GAC TCC T Asp Ser C	GC ATG ys Met	AAC Asn	673
GCC ACC AAC Ala Thr Asn 85	CAC GCC His Ala	ATC CTG Ile Leu 90	CAG TCC Gln Ser	CTG GTG Leu Val	CAC CTG A His Leu M 95	TG AAG et Lys	CCA Pro	721
AAC GCA GTC Asn Ala Val 100	COC AAG Pro Lys	GCG TGC Ala Cys 105	TGT GCA Cys Ala	CCC ACC Pro Thr 110	AAG CTG A Lys Leu S	GC GCC er Ala	ACC Thr 115	769
TCT GTG CTC Ser Val Leu	TAC TAT Tyr Tyr 120	Asp Ser	AGC AAC Ser Asn	AAC GTC Asn Val 125	ATC CTG C	GC AAG rg Lys 130	CAC His	817
CGC AAC ATG Arg Asn Met	GTG GTC Val Val 135	AAG GCC Lys Ala	TGC GGC Cys Gly 140	TGC CAC Cys His	TGAGTCAGC	C CGCC	CAGCCC	870
TACTECAGCC	ACCCTTCT	CA TCTGG	ATCGG GC	CCTGCAGA	GGCAGAAAA	C CCTT	AAATGC	930
TGTCACAGCT	CAAGCAGG	AG TGTCA	gegec cc	ТСАСТСТС	GGTGCCTAC	T TCCT	GTCAGG	990

1003

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14,

Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala
-139 -135 -130 / -125

Gly Glu Ala Val Thr Ala Ala Glu Phe Arg/IXe Tyr Lys Val Pro Ser
-120 -115 -110

Ile His Leu Leu Asn Arg Thr Leu His Wal Ser Met Phe Gln Val Val -105 -95

Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln
-90 -85 -80

Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala
-75 -65 -60

Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg
-55 -50 -45

Leu Tyr Val Glu Thr Gly Asp Gly His Ser Val Asp Pro Gly Leu Ala
-40 -35 -30

Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val

Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val

Arg Pro Leu Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln
10 15 20

Ala Asn Ard Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly 25 30 35

Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu 45 50

Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr

/55

60

65

Cys/Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr

Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala 90 95 100

51

Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val

Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn 120 125 130

Met Val Val Lys Ala Cys Gly Cys His 135 140

Je orna